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RAW SEQUENCE LISTING DATE: 02/22/2001
PATENT APPLICATION: US/09/776,874 TIME: 10:35:09

DATE: 02/22/2001
TIME: 10:35:09

Input Set : A:\Seq.txt
Output Set: N:\CRF3\02222001\I776874.raw

SEQUENCE LISTING

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/776,874

DATE: 02/22/2001
TIME: 10:35:09

Input Set : A:\Seq.txt
Output Set: N:\CRF3\02222001\I776874.raw

C--> 49 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
50 CCATCCTAAT ACGACTCACT ATAGGGC 27
52 (2) INFORMATION FOR SEQ ID NO: 2:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 24
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
C--> 58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
59 GTACTGATGC CATGTAAC TG AATC 24
61 (2) INFORMATION FOR SEQ ID NO: 3:
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 23
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: single
66 (D) TOPOLOGY: linear
C--> 67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
68 ACTCACTATA GGGCTCGAGC GGC 23
70 (2) INFORMATION FOR SEQ ID NO: 4:
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 22
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: linear
C--> 76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
77 GCATCTTAGC CGTCCTTCTT CG 22
79 (2) INFORMATION FOR SEQ ID NO: 5:
80 (i) SEQUENCE CHARACTERISTICS:
81 (A) LENGTH: 15
82 (B) TYPE: nucleic acid
83 (C) STRANDEDNESS: single
84 (D) TOPOLOGY: linear
C--> 85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
86 TTTTTTTTTT TTTTT 15
88 (2) INFORMATION FOR SEQ ID NO: 6:
89 (i) SEQUENCE CHARACTERISTICS:
90 (A) LENGTH: 23
91 (B) TYPE: nucleic acid
92 (C) STRANDEDNESS: single
93 (D) TOPOLOGY: linear
C--> 94 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
95 TTTCGATCCCC AGAAGGAATC AAC 23
97 (2) INFORMATION FOR SEQ ID NO: 7:
98 (i) SEQUENCE CHARACTERISTICS:
99 (A) LENGTH: 24
100 (B) TYPE: nucleic acid
101 (C) STRANDEDNESS: single
102 (D) TOPOLOGY: linear
C--> 103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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104 GTAGTGATGC CATGTAAC TG AAC T 24
106 (2) INFORMATION FOR SEQ ID NO: 8:
107 (i) SEQUENCE CHARACTERISTICS:
108 (A) LENGTH: 9
109 (B) TYPE: amino acid
110 (C) STRANDEDNESS: single
111 (D) TOPOLOGY: linear
C--> 112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
113 Tyr Gly Pro Asp Val Gly Gln Pro Arg
114 5 9
116 (2) INFORMATION FOR SEQ ID NO: 9:
117 (i) SEQUENCE CHARACTERISTICS:
118 (A) LENGTH: 1721
119 (B) TYPE: nucleic acid
120 (C) STRANDEDNESS: double
121 (D) TOPOLOGY: linear
C--> 122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
123 CTAGACCTT CGACTCTCCG CTGCCGCCA GCTGGCGGG GGAGCAGCCA GGTGAGGCCA 60
124 AGATGCTGCT GCGCTCGAAG CCTGCGCTGC CGCCGCCGCT GATGCTGCTG CTCCTGGGC 120
125 CGCTGGTCC CCTCTCCCT GCGCCCTGC CCCGACCTGC GAAGGCACAG GACGTCGTGG 180
C--> 126 ACCTGGACTT CTTCAACCCAG GAGCCGCTGC ACCTGGTGGAG CCCCTCGTTC CTGTCCTGCA 240
127 CCATTGAGGC CAACCTGGCC ACGGACCCGC GGTCCCTCAT CCTCTGGGT TCTCCAAAGC 300
128 TTCTGACCTT GCCCAGAGGC TTGTCCTCTG CGTACCTGAG GTTGGTGGC ACCAAGACAG 360
129 ACTTCCTAA TTTGATCCC AAGAAGGAAT CAACCTTGA AGAGAGAAAT TACTGGCAAT 420
130 CTCAAGTCAA CCAGGATTAT TGCAATATG GATCCATCCC TCTCTGATGTG GAGGAGAAAT 480
131 TACGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
132 TCAAGAACAG CACCTACTCA AGAAGCTCTG TAGATGTGCT ATACACTTTT GCAAACGTGCT 600
133 CAGGACTGGA CTTGATCTTT GGCTAAATG CGTATTAG AACAGCAGAT TTGCACTGGA 660
134 ACAGTTCTAA TGCTCAGTT CTCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTCTT 720
135 GGGAACTAGG CAATGAACTT AACAGTTTCC TAAAGAAGGC TGATATTTC ATCAATGGGT 780
136 CGCAGTAGG AGAAGATTAT ATTCAATTGC ATAATTCCTT AAGAAAGTCC ACCCTTAAAAA 840
137 ATGAAACT CTATGGCTC GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
138 AGAGCTCTT GAAGGCTGGT GGAGAAAGTGA TTGATTCTG TACATGGCAT CACTACTATT 960
139 TGAATGGACG GACTGCTACC AGGGAAAGATT TTCTAAACCC TGATGTATTG GACATTTTA 1020
140 TTTCATCTGT GCAAAGTTCA AAGAAGAGG TGAGAGTC CAGGCTGGC AAGAAGGTCT 1080
141 GGTTAGGAGA AACAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTG 1140
142 CAGCTGGCTT TATGTGCTG GATAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
143 TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTT ACTGGATGAA AACTTGGATC 1260
144 CTTTACCTGA TTATTGGCTA TCTCTTCTGT TCAAGAAATT GGTGGGCACC AAGGTGTTAA 1320
145 TGGCAAGCGT GCAAGGTTCA AAGAAGAGG AGCTTCAGT ATACCTTCAT TGACAAAACA 1380
146 CTGACAATCC AAGGTATAAA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCCATAACG 1440
147 TCACCAAGTA CTTGGCGTTA CCTATCCTT TTCTCAACAA GCAAGTGGAT AAATACCTTC 1500
148 TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAATCTGT CCAACTCAAT GGCTAACTC 1560
149 TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGG AAAACCTCTC CGGCCAGGAA 1620
150 GTTCACCTGGG CTTGGCCAGCT TTCTCATATA GTTTTTTGT GATAAGAAAT GCAAAGTTG 1680
151 CTGCTTGCACT CTGAAAATAA AATATACTAG TCTTGACACT G 1721
153 (2) INFORMATION FOR SEQ ID NO: 10:
154 (i) SEQUENCE CHARACTERISTICS:
155 (A) LENGTH: 543

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156 (B) TYPE: amino acid
157 (C) STRANDEDNESS: single
158 (D) TOPOLOGY: linear
C--> 159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
160 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
161 5 10 15
163 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
164 20 25 30
166 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
167 35 40 45
169 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
170 50 55 60
172 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
173 65 70 75 80
175 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
176 85 90 95
178 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
179 100 105 110
181 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
182 115 120 125
184 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
185 130 135 140
187 Pro Tyr Gin Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
188 145 150 155 160
190 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
191 165 170 175
193 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
194 180 185 190
196 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
197 195 200 205
199 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
200 210 215 220
202 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
203 225 230 235 240
205 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
206 245 250 255
208 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
209 260 265 270
211 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
212 275 280 285
214 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
215 290 295 300
217 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
218 305 310 315 320
220 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
221 325 330 335
223 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
224 340 345 350
226 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys

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227	355	360	365													
229	Leu	Gly	Leu	Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val
230	370	375	380													
232	Phe	Phe	Gly	Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro
233	385	390	395	400												
235	Leu	Pro	Asp	Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr
236	405	410	415													
238	Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg
239	420	425	430													
241	Val	Tyr	Leu	His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly
242	435	440	445													
244	Asp	Leu	Thr	Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu
245	450	455	460													
247	Arg	Leu	Pro	Tyr	Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu
248	465	470	475	480												
250	Arg	Pro	Leu	Gly	Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn
251	485	490	495													
253	Gly	Leu	Thr	Leu	Lys	Met	Val	Asp	Asp	Gln	Thr	Leu	Pro	Pro	Leu	Met
254	500	505	510													
256	Glu	Lys	Pro	Leu	Arg	Pro	Gly	Ser	Ser	Leu	Gly	Leu	Pro	Ala	Phe	Ser
257	515	520	525													
259	Tyr	Ser	Phe	Phe	Val	Ile	Arg	Asn	Ala	Lys	Val	Ala	Ala	Cys	Ile	
260	530	535	540	543												

262 (2) INFORMATION FOR SEQ ID NO: 11:

263 (i) SEQUENCE CHARACTERISTICS:

264 (A) LENGTH: 1721

265 (B) TYPE: nucleic acid

266 (C) STRANDEDNESS: double

267 (D) TOPOLOGY: linear

C--> 268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

270	CT	AGA	GCT	TTC	GAC	14												
272	TCT	CCG	CTG	CGC	GGC	AGC	TGG	CGG	GGG	GAG	CAG	CCA	GGT	GAG	CCC	AAG	62	
274	ATG	CTG	CTG	CGC	TCG	AAG	CCT	GCG	CTG	CCG	CCG	CTG	ATG	CTG	CTG	CTG	CTG	110
275	Met	Leu	Leu	Arg	Ser	Lys	Pro	Ala	Leu	Pro	Pro	Pro	Leu	Met	Leu	Leu		
276	5	10	15															
278	CTC	CTG	GGG	CCG	CTG	GGT	CCC	CTC	TCC	CCT	GGC	GCC	CTG	CCC	CGA	CCT	158	
279	Leu	Leu	Gly	Pro	Leu	Gly	Pro	Leu	Ser	Pro	Gly	Ala	Leu	Pro	Arg	Pro		
280	20	25	30															
282	GCG	CAA	GCA	CAG	GAC	GTC	GTG	GAC	CTG	GAC	TTC	TTC	ACC	CAG	GAG	CCG	206	
283	Ala	Gln	Ala	Gln	Asp	Val	Val	Asp	Leu	Asp	Phe	Phe	Thr	Gln	Glu	Pro		
284	35	40	45															
286	CTG	CAC	CTG	GTG	AGC	CCC	TCG	TTC	CTG	TCC	GTC	ACC	ATT	GAC	GCC	AAC	254	
287	Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn		
288	50	55	60															
290	CTG	GCC	ACG	GAC	CCG	CGG	TTC	CTC	ATC	CTC	CTG	GGT	TCT	CCA	AAG	CTT	302	
291	Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu		
292	65	70	75	80														
294	CGT	ACC	TTG	GCC	AGA	GCC	TTG	TCT	CCT	GCG	TAC	CTG	AGG	TTT	GGT	GGC	350	
295	Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	Gly		

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/776,874

DATE: 02/22/2001
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Input Set : A:\Seq.txt
Output Set: N:\CRF3\02222001\1776874.raw

L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:49 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:58 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:67 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:76 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:85 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:94 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:103 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:112 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:122 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:126 M:111 C: (47) String data converted to upper case,
L:159 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:268 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:418 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:441 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:482 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:480 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=14, value=[singl]
L:571 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:592 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=15
L:743 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:762 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:771 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:780 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:789 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:798 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:807 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:816 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:825 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:834 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:843 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:852 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:861 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:870 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:879 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:897 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:906 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:915 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:924 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:933 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:942 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:951 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:960 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:969 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:978 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:987 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]

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L:1893 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:]
L:1917 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=43
L:1949 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:]
L:2029 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:]
L:2093 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=45
L:2201 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:]
L:2217 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:]